On page 13, line 14, after "Ec107.", insert -- Seq. ID No.

42.--.

## IN THE CLAIMS

Please amend the claims as follows.

reverse transcriptase (RT) of claim 13 [which is capable of synthesizing msDNA], which RT [comprises] has a [conserved] sequence of amino acid residues as follows: Tyr-Xaa-Asp-Asp. wherein Xaa [tyrosine, x which] is alanine or cysteine[, and two aspartic acid residues], as shown in Seq. ID No. 4, residues 168-171.

[comprises] has a second [conserved] sequence of amino acid residues as follows: Ser-Xaa-Xaa<sub>1</sub>-Xaa<sub>2</sub>, wherein [serine, [x which Xaa is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine and isoleucine, [x<sub>1</sub> which] Xaa<sub>1</sub> is a polar residue selected from the group consisting of threonine, asparagine, lysine and serine and [x<sub>2</sub> which] Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine and alanine, as shown in Seq. ID No. 4, residues 96-99.

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- (Amended) The bacterial RT of claim 2 which [comprises] has a third [conserved] sequence of amino acid residues as follows: Asn-Xaa-Xaa<sub>1</sub>, wherein [asparagine, x which] Xaa is a hydrophobic residue selected from the group consisting of alanine, leucine and phenylalanine and  $[x_1 \text{ which}]$  Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of leucine, valine and isoleucine.
  - 4. (Amended) The bacterial RT of claim 3 which [comprises] has a fourth [conserved] sequence of amino acid residues as follows: Xaa-Val-Thr-Gly, wherein Xaa [x which] is a polar residue selected from the group consisting of arginine, glutamic acid, lysine, valine and glutamine[, a second residue which is valine, a third residue which is threonine and a fourth residue which is glycine], as shown in Seq. ID No. 4, residues 225-228.
    - 5. (Amended) The bacterial RT of claim 1 which has the common subdomains 1 through 7 shown in [Table 5] Figure 14.
    - 6. (Amended) The bacterial RT of claim 1 wherein the [conserved] sequence is located in subdomain 5 shown in [Table 5]

(Amended) The bacterial RT of claim 6 which has [a two or constructions are total of] the 61 conserved amino acid residues as shown by black

SUITE,650 230 SO, FÖTTEENTH ST. PHILADELPHIA, PA 19102 (215) 875-8383 dots in Figure 14, wherein h is a hydrophobic residue and p is a small polar residue.

8. (Amended) An isolated and purified bacterial RT which comprises [al an amino acid sequence [of amino acid residues] selected from the sequences shown in Figure 14, which sequences are shown in Seq. ID Nos. 30-36.

Please add the following claims.

which the amino acid sequences Tyr-Xaa-Asp-Asp, Ser-Xaa-Xaa<sub>1</sub>-Xaa<sub>2</sub>,
Asn-Xaa-Xaa<sub>1</sub>, and Xaa-Val-Thr-Gly are arranged in order starting
from the amino terminal end of the RT.

13. An isolated and purified bacterial reverse transcriptase (RT) which synthesizes msDNA, and which is essential for the synthesis of msDNA in vivo.--

## REMARKS

Applicants submit this Amendment in response to the Office Action of March 5, 1996.

Preliminarily, Applicants note that claims 1-11 are currently pending in the application. The Examiner has mistakenly indicated on the Office Action Summary Sheet that claims 1-10 are pending.

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